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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:18:43 ; Search time 3175 seconds
(without alignments)
1668.255 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182

Sequence: 1 gagctgcctccccgcgtc.....tgactgtggacaggctagc 182

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
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- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	182	100.0	5270	12	AF176637	AF176637 Plastid t
2	111.2	61.1	168	6	AX076661	AX076661 Sequence
3	85.8	47.1	127	6	AX137514	AX137514 Sequence
4	85.8	47.1	127	6	E51179	E51179 Method for
5	85.8	47.1	127	6	E51197	E51197 Process for
6	85.8	47.1	766	8	TOBCTGVR	J01453 Tobacco (N.
7	85.8	47.1	2113	8	CHNTRN1	V00165 Tobacco chl.
8	85.8	47.1	3274	8	CHNPRNVI	X70938 N.plumbagin
C 9	85.8	47.1	7829	8	CPY18934	X18934 Solanum nlg
10	85.8	47.1	155939	8	CHNTXX	Z00044 Nicotiana t
C 11	85.8	47.1	155939	8	CHNTXX	Z00044 Nicotiana t
12	85.8	47.1	156687	8	ABE316582	AJ316582 Atropa be
C 13	85.8	47.1	156687	8	ABE316582	AJ316582 Atropa be
14	85.4	46.9	184	6	AR145914	AJ145914 Sequence
15	85.4	46.9	300	6	AR171710	AR171710 Sequence
16	85.4	46.9	300	6	AR171711	AR171711 Sequence
C 17	85.4	46.9	2962	12	XXU12809	U12809 Transform
C 18	85.4	46.9	3019	12	XXU12810	U12810 Transform
C 19	85.4	46.9	3019	12	XXU12811	U12811 Transform
C 20	85.4	46.9	3136	12	AF061065	AF061065 Plastid t
C 21	85.4	46.9	4126	12	XXU12814	U12814 Transform
C 22	85.4	46.9	4126	12	XXU12815	U12815 Transform
C 23	85.4	46.9	4174	12	XXU12812	U12812 Transform
C 24	85.4	46.9	4174	12	XXU12813	U12813 Transform
C 25	85.4	46.9	4304	12	AY005806	AY005806 Transform
C 26	85.4	46.9	7454	12	CTR312391	AJ312391 Chloropia
C 27	85.4	46.9	7626	12	CTR312392	AJ312392 Chloropia
C 28	85.4	46.9	7626	12	CTR312393	AJ312393 Chloropia
29	84.8	46.6	159	12	M23201	M23201 Synthetic c
30	84.8	46.6	310	12	M23200	M23200 Synthetic c
31	84.8	46.6	2731	1	PET31F1P	X62498 E.coli plas
32	84.8	46.6	2829	12	CVRSET5C	X54204 Cloning vec
33	84.8	46.6	2829	12	CVRSET6C	X54208 Cloning vec
34	84.8	46.6	2830	12	CVRSET5B	X54203 Cloning vec
35	84.8	46.6	2830	12	CVRSET6B	X54207 Cloning vec
36	84.8	46.6	2831	12	CVRSET5A	X54202 Cloning vec
37	84.8	46.6	2831	12	CVRSET6A	X54206 Cloning vec
38	84.8	46.6	2894	12	CVR7NDE	U25269 Expression
39	84.8	46.6	3984	6	I15353	I15353 Sequence 1
C 40	84.8	46.6	3993	12	CVFGEEX1	X65317 Cloning vec
C 41	84.8	46.6	3995	12	CVFGEEX2	X65318 Cloning vec
42	84.8	46.6	5231	6	AX001273	AX001273 Sequence
43	84.8	46.6	5953	6	AX191649	AX191649 Sequence
44	84.8	46.6	39937	7	T7CG	V01146 Genome of b
45	83.2	45.7	187	6	AR004778	AR004778 Sequence

ALIGNMENTS

RESULT 1
AF176637/c
LOCUS AF176637 5270 bp DNA linear SYN 24-APR-2000
DEFINITION Plastid transformation vector pMSK49 plastid targeting region.
ACCESSION AF176637
VERSION AF176637.1 GI:7637848
KEYWORDS
SOURCE Plastid transformation vector pMSK49.
ORGANISM Plastid transformation vector pMSK49
artificial sequences; vectors.
REFERENCE
1 (bases 1 to 5270)
Khan,M.S. and Maliga,P.
Fluorescent antibiotic-resistance marker for tracking plastid
transformation in higher plants
Nat. Biotechnol. 17 (9), 910-915 (1999)
JOURNAL

99403345
10471936
PUBMED
REFERENCE
2 (bases 1 to 5270)
Khan, M.S. and Maliga, P.
Direct Submission
Submitted (09-AUG-1999) Waksman Institute, Rutgers University, 190
Frelinhuyzen Road, Piscataway, NJ 08854, USA

FEATURES
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/organism="Plastid transformation vector pMSK49"
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3880..5270
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complement(1..1332)
/product="16S ribosomal RNA"
complement(1564..1635)
/product="rRNA-Val"
1885..1910
/note="ClaI and HindIII restriction sites"
1911..2099
/gene="psbA"
complement(1911..2099)
2100..2110
/note="contains XbaI restriction site"
complement(2111..3712)
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complement(2111..3712)
/gene="aadA11gfp-S3"
/note="adenyltransferase fused at its
C-terminus via the 11-mer ELAVEGKLEVA with the soluble
modified form of the Acetivora victoria green fluorescent
protein with Genbank Accession Number U70495; N-terminal
segment is the T7 phage gene 10 N-terminus"
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TGKLPADVAADAMERLPAQYQVILEARQAYLGQEDRLASRQDLFEVHYKGE
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GKTLKFTCTTGKLPVWPPTLVTTFSYGVQCFSPYDPMKRHDFFKSAPEGVQENT
ISPKDGNKYTRAQVKEFGDTLVNRIELKIDFKEDGNILGHKLEYNYNSHNYITAD
KKNKIRANFKIRINIEDGSVOLADHYQNTPTIGDGPVLLPDNHYLSTQSALSKDPE
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/note="Region: C-myc tag"
complement(2864..3646)
/gene="aadA11gfp-S3"
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complement(2831..2863)
/gene="aadA11gfp-S3"
/note="Region: 11-mer joining segment ELAVEGKLEVA"
complement(2114..2830)
/gene="aadA11gfp-S3"
/note="Region: green fluorescent protein"

misc_feature
AX076661 168 bp DNA linear PAT 06-FEB-2001
Sequence 1 from Patent WO0104331.
ACCESSION AX076661
VERSION AX076661.1 GI:12711193
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Calgene LLC (US)
FEATURES
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/db_xref="taxon:32644"
41 t

BASE COUNT 45 a 31 c 51 g 41 t
ORIGIN

Query Match 61.1%; Score 111.2; DB 6; Length 168;
Best Local Similarity 88.7%; Pred. No. 5.1e-25;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;

QY 7 GCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTGAGGGG 66
Db 23 GCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTGAGGGG 82

QY 67 CAGGATGGCTATATTTCTGGGAGGAGACACACACGGTTTCCCACTAGAAATAATTTG 126
Db 83 CAGGATGGCTATATTTCTGGGAGGCGA---ACTCCGGGCGAATTTGAGAAATAATTTG 138

QY 127 TTTAACTTTAAGAAGGAGATATACATATGG 156
Db 139 TTTAACTTTAAGAAGGAGATATACCATGG 168

RESULT 3
LOCUS AX137514
DEFINITION Sequence 16 from Patent EP1076095.
ACCESSION AX137514

misc_feature complement(3683..3858)
/note="Prin17g10-DB/EC promoter and translation control
region contained in SacI-NheI fragment."
3859..3879
/note="SacI, EcoRI and PstI restriction sites"
BASE COUNT 1378 a 1330 c 1145 g 1417 t
ORIGIN

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Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCTCGCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTG 60
Db 3864 GAGCTCGCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTG 3805

QY 61 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACACACACGGTTTCCCACTAGAAATA 120
Db 3804 AGGGGCGAGGATGGCTATATTTCTGGGAGGAGACACACACGGTTTCCCACTAGAAATA 3745

QY 121 ATTTCGTTTAACTTTAAGAAGGAGATATACATATGCAAGCATGACTGGTGACAGGCTA 180
Db 3744 ATTTCGTTTAACTTTAAGAAGGAGATATACATATGCAAGCATGACTGGTGACAGGCTA 3685

QY 181 GC 182
Db 3684 GC 3683

RESULT 2
LOCUS AX076661
DEFINITION Sequence 1 from Patent WO0104331.
ACCESSION AX076661
VERSION AX076661.1 GI:12711193
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Calgene LLC (US)
FEATURES
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41 t

BASE COUNT 45 a 31 c 51 g 41 t
ORIGIN

Query Match 61.1%; Score 111.2; DB 6; Length 168;
Best Local Similarity 88.7%; Pred. No. 5.1e-25;
Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;

QY 7 GCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTGAGGGG 66
Db 23 GCTCCCGCCGCGTTCATGAGATGGATAGAGCTCGTGGGATTGACGTGAGGGG 82

QY 67 CAGGATGGCTATATTTCTGGGAGGAGACACACACGGTTTCCCACTAGAAATAATTTG 126
Db 83 CAGGATGGCTATATTTCTGGGAGGCGA---ACTCCGGGCGAATTTGAGAAATAATTTG 138

QY 127 TTTAACTTTAAGAAGGAGATATACATATGG 156
Db 139 TTTAACTTTAAGAAGGAGATATACCATGG 168

RESULT 3
LOCUS AX137514
DEFINITION Sequence 16 from Patent EP1076095.
ACCESSION AX137514

Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA		47.1%; Score 85.8; DB 8; Length 2113;	
Nucleic Acids Res. 9 (20), 5399-5406 (1981)		Pred. No. 1e-16; Mismatches 0; Caps 0;	
82059514		Conservative	
7029469			
rRNA sequence contributed on tape April 1983 by M. Sprinzl & D.H. Gauss; from their entry 2063 in Nucleic Acids Res. 11, r55-r103 (1983). [1] proposes bases 302 or 308 as possible sites for transcription initiation, based on an in vitro assay with E.coli RNA polymerase.			
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/organelle="plastid:chloroplast"			
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/note="codon recognized: GUC: Val-tRNA (NAR: 2063)"			
628..>766			
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200 a 145 c 215 g 206 t			
BstEII site.			
Query Match		47.1%; Score 85.8; DB 8; Length 766;	
Best Local Similarity		97.8%; Pred. No. 9.3e-17;	
Matches		87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
5 TCGTCTCCCGCCGCTTCATGAGATGATGAAGAGGCTCGTGGGATTGACGTGAGG 64			
429 TTGCTCCCGCCGCTTCATGAGATGATGAAGAGGCTCGTGGGATTGACGTGAGG 488			
65 GCGAGGATGGCTATATTCTGGGAGGA 93			
489 GCGAGGATGGCTATATTCTGGGAGGA 517			
RESULT 7			
CHNTRN1		2113 bp DNA linear PLN 31-MAR-1992	
LOCUS		Tobacco chloroplast genes for 16S ribosomal RNA and trNA-Val.	
DEFINITION		V00165 J01453	
FEATURES		16S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val. common tobacco.	
ORGANISM		Chloroplast Nicotiana tabacum	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.	
AUTHORS		1 (bases 628 to 2113)	
TITLE		Tobacco chloroplast genes for 16S ribosomal RNA and trNA-Val.	
JOURNAL		Tobacco chloroplast DNA	
MEDLINE		Gene 17 (2), 213-218 (1982)	
PUBLISHED		7044901	
REFERENCE		2 (bases 1 to 766)	
AUTHORS		Tobacco chloroplast DNA	
TITLE		Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA	
JOURNAL		Nucleic Acids Res. 9 (20), 5399-5406 (1981)	
MEDLINE		82059514	
PUBLISHED		7029469	
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Best Local Similarity 97.8%; Pred. No. 1.le-16;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1028 TTGCTCCCCCGCTCGTTCATGAGATGATGATAAGAGGCTCGTGGGATTCACGTGAGGG 1087
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QY 65 GGCAGGATGGCTATATTTCTGGGAGGGA 93
Db 1088 GGCAGGATGGCTATATTTCTGGGAGGGA 1116
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RESULT 9
CPY18934/c
LOCUS
DEFINITION Solanum nigrum chloroplast tRNA-Ala, tRNA-Ile, 16S rRNA, tRNA-Val,
rps12, rps7, ndhB genes.
ACCESSION Y18934
VERSION Y18934.1 GI:4688654
KEYWORDS 16S ribosomal RNA; 16S rRNA gene; NADH dehydrogenase subunit; ndhB
gene; ribosomal protein S12; ribosomal protein S7; rps12 gene; rps7
gene; transfer RNA-Ala; transfer RNA-Ile; transfer RNA-Val;
tRNA-Ala gene; tRNA-Ile gene; tRNA-Val gene.
SOURCE black nightshade.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 7829)
AUTHORS Kavanagh,T.A., Thanh,N.D., Lao,N.T., McGrath,N., Peter,S.O.,
Horvath,E.M., Dix,P.J. and Medgyesy,P.
TITLE Homeologous plastid DNA transformation in tobacco is mediated by
multiple recombination events
JOURNAL Genetics 152 (3), 1111-1122 (1999)
MEDLINE 99318845
PUBMED 10388829
REFERENCE 2 (bases 1 to 7829)
AUTHORS Kavanagh,T.A.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1999) T.A. Kavanagh, University of Dublin,
Department of Genetics, Trinity College, Dublin 2, IRELAND
FEATURES
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QY 5 TCGCTCCCCCGCTCGTTCATGAGATGATGATAAGAGGCTCGTGGGATTCACGTGAGGG 64
Db 1028 TTGCTCCCCCGCTCGTTCATGAGATGATGATAAGAGGCTCGTGGGATTCACGTGAGGG 64
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QY 65 GGCAGGATGGCTATATTTCTGGGAGGGA 93
Db 3708 GGCAGGATGGCTATATTTCTGGGAGGGA 3680
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Query Match 47.1%; Score 85.8; DB 8; Length 7829;
Best Local Similarity 97.8%; Pred. No. 1.2e-16;
Matches 87; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCGCTCCCCCGCTCGTTCATGAGATGATGATAAGAGGCTCGTGGGATTCACGTGAGGG 64
Db 3768 TTGCTCCCCCGCTCGTTCATGAGATGATGATAAGAGGCTCGTGGGATTCACGTGAGGG 3709
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QY 65 GGCAGGATGGCTATATTTCTGGGAGGGA 93
Db 3708 GGCAGGATGGCTATATTTCTGGGAGGGA 3680
|||||

RESULT 10
CHNTXX
LOCUS
DEFINITION Nicotiana tabacum chloroplast genome DNA.
ACCESSION Z00044.S54304
VERSION Z00044.1 GI:2924257
KEYWORDS 16S ribosomal RNA; 23S ribosomal RNA; 4.5S ribosomal RNA; 5S
ribosomal RNA; acetyl-CoA carboxylase; ATP synthase; ATP-dependent
protease; autonomous replication; chloroplast; circular; complete
genome; cytochrome b/f complex; cytochrome b6; cytochrome f;
initiation factor; inverted repeat; maturase; NADH dehydrogenase;
PSI 9kD protein; PSI I-protein; PSI J-protein; PSI 700 apoprotein;
PSII 10kD phosphoprotein; PSII 32kD protein; PSII 44kD protein;
PSII 47kD protein; PSII cytochrome b559; PSII L2 protein; PSII
I-protein; PSII J-protein; PSII K-protein; PSII L-protein; PSII
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JOURNAL
COMMENT

		gene; petL gene; petN gene; potential heme-binding protein; PSI P700 apoprotein A1; psaA gene; psab gene; psac gene; psai gene; psaa gene; psba gene; psbb gene; psbc gene; psbd gene; psbe gene; psbf gene; psbg gene; psbh gene; psbi gene; psbj gene; psbk gene; psbl gene; psbm gene; psbn gene; psbt gene; psi 9kD protein; psi p700 apoprotein A2; psi reaction center subunit VIII; psi 10kD phosphophorprotein; PSII 32kd protein; PSII 44kd protein; PSII 47KD protein; PSII D2 protein; PSII I protein; PSII K protein; PSII M protein; PSII N-protein; PSII reaction center subunit IX; PSII reaction center subunit V; PSII reaction center subunit VII; PSII T-protein; rbcL gene; ribosomal protein L16; ribosomal protein L18; ribosomal protein L2; ribosomal protein L20; ribosomal protein L21; ribosomal protein L22; ribosomal protein L23; ribosomal protein L24; ribosomal protein L25; ribosomal protein L26; ribosomal protein L27; ribosomal protein L28; ribosomal protein L29; ribosomal protein L30; ribosomal protein L31; ribosomal protein L32; ribosomal protein L33; ribosomal protein L34; ribosomal protein L35; ribosomal protein S12; ribosomal protein S16; ribosomal protein S18; ribosomal protein S19; ribosomal protein S2; ribosomal protein S3; RNA polymerase alpha subunit; RNA polymerase beta' subunit; rpl14 gene; rpl16 gene; rpl2 gene; rpl20 gene; rpl22 gene; rpoB gene; rpoC1 gene; rpoC2 gene; rps11 gene; rps12 gene; rps14 gene; rps15 gene; rps16 gene; rps18 gene; rps19 gene; rps2 gene; rps3 gene; rps4 gene; rps7 gene; rps8 gene; rnl16 gene; rln23 gene; rln4-5 gene; rln5 gene; rubisco large subunit; transfer RNA-Ala(UCC); transfer RNA-Arg(ACG); transfer RNA-Arg(UUC) transfer RNA-Asn(GUU); transfer RNA-Asp(GUG); transfer RNA-Cys(GCA); transfer RNA-Fm(CAU); transfer RNA-Gln (UUG); transfer RNA-Glu(UUC); transfer RNA-His(GUG); transfer RNA-Ile(GGC); transfer RNA-Leu(CAA); transfer RNA-Lys(UUU); transfer (UAG); transfer RNA-Met(CAU); transfer RNA-Phe(CAA); transfer RNA-Pro(UGC); transfer RNA-Ser(UCU); transfer RNA-Thr(UGU); transfer RNA-Trp(CCA); transfer RNA-Tyr(GUA); transfer RNA-Val (GUU); transfer RNA-Val(GAC); trna-Ala(UCC) gene; trna-Arg(GUC) gene; trna-Arg(UCU) gene; trna-fm(CAU) gene; trna-gln(UUG) gene; trna-Cys(GCG) gene; trna-gly(UCC) gene; trna-Ile(AUA) gene; trna-His(GUG) gene; trna-leu(CAU) gene; trna-leu(UAG) gene; trna-Leu(CAA) gene; trna-Leu(UAA) gene; trna-Phe(GAA) gene; trna-Lys(UUU) gene; trna-met(CAU) gene; trna-ser(UCU) gene; trna-Pro(UGG) gene; trna-ser(SGI) gene; trna-thl(GGU) gene; trna-Ser(UGA) gene; trna-Tyr(GUA) gene; trna-val(GUC) gene; trna-trp(CCA) gene; ycf1 protein; ycf1 gene; ycf1 protein; ycf15 gene; ycf15 protein; ycf12 gene; ycf2 protein; ycf3 protein; ycf3 protein; ycf4 gene; ycf9 gene; ycf9 protein.	
	SOURCE	belladonna	
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	REFERENCE	Asteridae; euasterids I; Solanaceae; Atropa belladonna C., Regel,R., Gila Du,T., Hupfer,H., Herrmann,R.G. and Maier,R.M. The nucleotide sequence of the plastid chromosome of Atropa belladonna (deadly nightshade) and its comparison with that of Nicotiana tabacum with emphasis on sequence elements relevant for microevolution Unpublished 2 (bases 1 to 156687)	
	JOURNAL	Schmitz-Linneweber,C.	
	REFERENCE	Schmitz-Linneweber,C.	
	TITLE	Direct Submission	
	JOURNAL	Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches Institut, Ludwig Maximilians Universität München, Menzinger Str 67, München, Bavaria 80638, Germany	
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DEFINITION Sequence 3 from patent US 6218145.
ACCESSION ARI45914
VERSION ARI45914.1 GI:15109103
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 184)
AUTHORS Bogosian,G., O'Neil,J.P. and Staub,J.M.
TITLE Bacterial expression systems based on plactic or mitochondrial
promoter combinations
JOURNAL Patent: US 6218145-A 3 17-APR-2001;
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BASE COUNT 49 a 33 c 59 g 43 t
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Mon Dec 16 13:20:21 2002

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ACCESSION ARI17170
VERSION   ARI17170.1  GI:17910660
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SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 300)
AUTHORS  Maliga,P., Carrier,H. and Chaudhuri,S.
TITLE     Editing-based selectable plastid marker genes
JOURNAL   Patent: US 6297054-A 4 02-OCT-2001;
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Job time : 3319 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:17:53 ; Search time 307 Seconds

(without alignments)
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Title: US-09-762-105-14

Perfect score: 182

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	182	100.0	182	21	AAZ61373 Nucleotide sequenc
2	182	100.0	1961	21	AAZ61384 Nucleotide sequenc
3	182	100.0	5263	21	AAZ61386 Nucleotide sequenc
4	164.4	90.3	182	21	AAZ61374 Nucleotide sequenc
5	159.4	87.6	161	21	AAZ61375 Nucleotide sequenc
6	111.2	61.1	168	21	AAZ68175 Prn/G10L fusion n
7	111.2	61.1	168	22	AAZ625352 Nucleotide sequenc
8	111.2	61.1	168	22	AAZ57902 Prn/G10L promoter
9	93.6	51.4	191	21	AAZ61361 Nucleotide sequenc

10	93.6	51.4	227	21	AAZ61360 Nucleotide sequenc
11	93.6	51.4	227	21	AAZ61362 Nucleotide sequenc
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14	92.2	50.7	183	21	AAZ61369 Nucleotide sequenc
15	92.2	50.7	185	21	AAZ61372 Nucleotide sequenc
16	92.2	50.7	195	21	AAZ61368 Nucleotide sequenc
17	90	49.5	130	22	AAZ61256 Plasmid rRNA opero
18	90	49.5	131	22	AAZ61259 Plasmid rRNA opero
19	90	49.5	154	21	AAZ61384 Nucleotide sequenc
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26	89	48.9	183	21	AAZ61371 Nucleotide sequenc
27	89	48.9	201	21	AAZ61370 Nucleotide sequenc
28	86.4	47.5	129	20	AAZ61430 Regulatory region
29	86	47.3	140	20	AAZ61424 5' and 3' regulato
30	86	47.3	164	20	AAZ61431 Regulatory region
31	85.8	47.1	127	22	AAZ61426 Plasmid 16S rRNA p
32	85.8	47.1	201	18	AAZ66301 DNA of upstream re
33	85.8	47.1	6477	22	AAZ61697 Chloroplast gene t
34	85.4	46.9	161	20	AAZ61423 5' and 3' regulato
35	85.4	46.9	165	20	AAZ61409 Prn promoter sequ
36	85.4	46.9	168	20	AAZ61407 Prn/rbcL/Rubisco
37	85.4	46.9	184	22	AAZ69143 Tobacco plastid RR
38	85.4	46.9	258	20	AAZ61429 Regulatory region
39	85.4	46.9	1134	18	AAZ65195 Plasmid targeting
40	85.4	46.9	1134	20	AAZ61415 Selectable marker
41	85.4	46.9	1183	21	AAZ61376 Nucleotide sequenc
42	85.4	46.9	1208	20	AAZ61433 Regulatory region
43	85.4	46.9	1416	20	AAZ61432 Regulatory region
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ALIGNMENTS

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XX AAZ61373;

AC AAZ61373;

XX 19-JUN-2000 (first entry)

DT Nucleotide sequence of chimeric promoter PrnLT7g10+DB/Ec.

DE Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;

XX Prn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.

KW Synthetic.

XX Key

OS Key

PH Key

FT Key

FT Key

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Db 181 GC 182
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ID AAZ61386 standard; DNA; 5263 BP.
XX AC AAZ61386;
XX 19-JUN-2000 (first entry)
XX Nucleotide sequence of plasmid pMSK49.
DE aada; protein expression; vaccine; haemoglobin; enzyme; psbA;
XX T7 phage gene 10; downstream box; green fluorescent protein; ss.
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XX 17-FEB-2000.
XX 03-AUG-1999; 99WO-US17806.
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX Disclosure; Fig 34A-B; 164pp; English.
XX The present sequence represents a vector of the invention. The
XX specification describes recombinant DNA constructs for expressing
XX heterologous proteins in the plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
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Db 3677 GC 3676
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XX AC AAZ61374;
XX 19-JUN-2000 (first entry)
XX Nucleotide sequence of chimeric promoter PrnLT7g10+DB/pt.
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
XX Prn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
XX Synthetic.
XX Key Location/Qualifiers
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XX WO200007431-A1.
XX 17-FEB-2000.
XX 03-AUG-1999; 99WO-US17806.
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX Maliga P, Kuroda H, Khan MS;
XX WPI; 2000-205525/18.
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX Disclosure; Fig 34A-B; 164pp; English.
XX The present sequence represents a vector of the invention. The
XX specification describes recombinant DNA constructs for expressing
XX heterologous proteins in the plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
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DT 05-JUN-2001 (first entry)
XX
DE DNA fragment designed for CRE-induced expression of recombinant protein.
XX
KW CRE recombinase; plastid genome manipulation;
KW site-specific recombination; ds.
XX
OS Synthetic.
XX
PN WO200121768-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US25930.
XX
PR 21-SEP-1999; 99US-0155007.
PR 13-JUN-2000; 2000US-0211139.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Malliga P, Cornelle S, Lutz K;
XX
XX WPI; 2001-266071/27.
XX
DR Removing target nucleic acid sequences e.g. selectable marker genes,
PT genes involved in plant cell metabolism, growth development and
PT fertility from plastid genomes, by Cre-mediated site specific
PT recombination -
XX
PS Example 3; Page 48; 83pp; English.
XX
CC The present sequence was used in an example illustrating an invention
CC relating to a method for manipulating the genome of higher plants. The
CC method involves selecting plant cells expressing proteins encoded by a
CC DNA construct having a nucleic acid encoding a marker, excision sites
CC and plastid targeting sequence for homologous recombination into a
CC plastid genome at a target sequence. The method is useful for removing
CC heterologous sequences from the plastid genome, such as selectable
CC marker genes following successful isolation of transformed progeny,
CC and for removing endogenous genes associated with male sterility, clpp
CC ribosomal proteins and ribosomal RNA operon sequences from the plastid
CC genome.
XX
XX Sequence 1049 BP; 269 A; 235 C; 282 G; 263 T; 0 other;
Query Match 51.4%; Score 93.6; DB 22; Length 1049;
Best Local Similarity 75.0%; Pred. No. 5.4e-21;
Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 GAGCTCGCTCCCGCGGTTCATGAGATGGATAAGAGGCTCGTGGGATTGACGTG 60
Db 1 GAGCTCGCTCCCGCGGTTCATGAGATGGATAAGAGGCTCGTGGGATTGACGTG 60

Qy 61 AGGGGCGAGGATGCTATATTTCTGGGCGGAGACACACCGTTTCCCACTAGAAATA 120
Db 61 AGGGGCGAGGATGCTATATTTCTGGGCGGAGATTAACCGATCGACGTGCAAGCGGACATT 120

Qy 121 ATTTTGTTTTAACTTAAAGAGGAGATATACATATGG 156
Db 121 TATTTTAAATTCGATAATTTTGTGCAAAACAATTTCG 156

RESULT 13
AA61382

ID AAZ61382 standard; DNA; 1985 BP.
XX
AC AAZ61382;
XX
DT 19-JUN-2000 (first entry)
XX
DE Nucleotide sequence of DNA construct FLARE16-S2.
XX
KW Green fluorescent protein; GFP; aadA; aptB; protein expression; vaccine;
KW haemoglobin; enzyme; psbA; ss.
XX
OS Synthetic.
OS Unidentified.
OS Aequorea victoria.
XX
PR Key Location/Qualifiers
FT misc_feature 7..221
FT /*tag= a
FT /note= "atpB downstream box"
FT 228..1010
FT /*tag= b
FT /note= "aadA sequence"
FT 1059..1779
FT /*tag= c
FT /note= "green fluorescent protein region"
FT 1790..1978
FT /*tag= d
FT /note= "psbA region"
XX
PN WO200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
PR 03-AUG-1998; 98US-0095167.
PR 15-DEC-1998; 98US-0112257.
PR 29-APR-1999; 99US-0131611.
PR 11-JUN-1999; 99US-0138764.
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Malliga P, Kuroda H, Khan MS;
XX
XX WPI; 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
PT heterologous protein in plastids of higher plants, includes promoter, a
PT leader sequence and a downstream box element -
XX
XX Disclosure; Fig 30; 164pp; English.
XX
XX The present sequence represents a DNA construct of the invention.
CC The specification describes recombinant DNA constructs for expressing
CC heterologous proteins in the plastids of higher plants. The DNA
CC constructs comprise a 5' regulatory region which includes a promoter
CC element, a leader sequence and a downstream box element operably linked
CC to a coding region of the heterologous protein. The chimeric regulatory
CC region enhances translational efficiency of an mRNA molecule encoded by
CC the DNA construct. The DNA constructs are used for producing transformed
CC monocol and dicot plants having high levels of heterologous protein
CC expression. They can be used to drive expression of proteins with
CC agronomic, industrial or pharmaceutical importance, including production
CC of vaccines, healthcare products like human haemoglobin, industrial or
CC household enzymes. Plants which can be transformed with the constructs
CC of the invention include maize, millet, sorghum, sugar cane, rice,
CC wheat, barley, oat, rye or turf grass.
XX
XX Sequence 1985 BP; 553 A; 431 C; 482 G; 519 T; 0 other;
Query Match 51.4%; Score 93.6; DB 21; Length 1985;
Best Local Similarity 75.0%; Pred. No. 6.9e-21;

Mon Dec 16 13:20:22 2002

heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing protein monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.

XX Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;

SQ Query Match 50.7%; Score 92.2; DB 21; Length 185;
Best Local Similarity 88.5%; Pred. No. 8.1e-21;
Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 GAGCTCGCTCCCGCCGCGCTTCATGAGATGATGAGAGGCTCGTGGGATTGACGTG 60

DB 1 GAGCTCGCTCCCGCCGCGCTTCATGAGATGATGAGAGGCTCGTGGGATTGACGTG 60

OY 61 AGGGGGCAGGATGGCTATATTTCTGGGAGGACCAACGCTTCCCACT 113

DB 61 AGGGGGCAGGATGGCTATATTTCTGGGAGGACCAACGCTTCCCACTTCTATT 113

Search completed: December 15, 2002, 00:32:45
Job time : 311 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:26:03 ; Search time 67 seconds
(without alignments)
833.062 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182

Sequence: 1 gagctgcctcccccgcgtc.....tgactggtgacaggctagc 182

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.6	49.2	171	1	US-08-217-360-16
2	86.4	47.5	129	2	US-08-189-256A-25
3	86.4	47.5	129	4	US-09-193-853-25
4	86	47.3	140	2	US-08-189-256A-19
5	86	47.3	140	4	US-09-193-853-19
6	86	47.3	164	2	US-08-189-256A-26
7	86	47.3	164	4	US-09-193-853-26
8	85.4	46.9	161	2	US-08-189-256A-18
9	85.4	46.9	161	4	US-09-193-853-18
10	85.4	46.9	165	2	US-08-189-256A-4
11	85.4	46.9	165	4	US-09-193-853-4
12	85.4	46.9	168	2	US-08-189-256A-2
13	85.4	46.9	168	4	US-09-193-853-2
14	85.4	46.9	184	4	US-08-283-419-3
15	85.4	46.9	258	2	US-08-189-256A-24
16	85.4	46.9	258	4	US-09-193-853-24
17	85.4	46.9	300	4	US-09-202-316-4
18	85.4	46.9	300	4	US-09-202-316-7
19	85.4	46.9	1134	2	US-08-189-256A-10
20	85.4	46.9	1134	4	US-09-193-853-10
21	85.4	46.9	1143	4	US-09-142-114B-6
22	85.4	46.9	1208	2	US-08-189-256A-28
23	85.4	46.9	1208	4	US-09-193-853-28
24	85.4	46.9	1416	2	US-08-189-256A-27
25	85.4	46.9	1416	4	US-09-193-853-27
26	85.4	46.9	1417	4	US-09-142-114B-7
27	85.4	46.9	2962	2	US-08-189-256A-3

c	28	85.4	46.9	2962	4	US-09-193-853-3	Sequence 3, Appli
	29	84.8	46.6	3984	1	US-08-040-753-1	Sequence 1, Appli
	30	83.8	46.0	105	4	US-09-597-877-9	Sequence 9, Appli
	31	83.2	45.7	187	1	US-08-096-182A-7	Sequence 7, Appli
	32	83.2	45.7	187	1	US-08-877-109-7	Sequence 7, Appli
	33	83.2	45.7	187	3	US-08-798-760-7	Sequence 7, Appli
	34	83.2	45.7	187	5	PCT-US94-08327-7	Sequence 7, Appli
	35	83	45.6	139	1	US-08-217-360-13	Sequence 13, Appli
	36	83	45.6	146	1	US-08-217-360-17	Sequence 17, Appli
	37	82.8	45.5	104	2	US-08-722-806A-9	Sequence 9, Appli
	38	82.8	45.5	104	4	US-09-337-028-9	Sequence 9, Appli
	39	82.2	45.2	150	2	US-08-189-256A-1	Sequence 1, Appli
	40	82.2	45.2	150	4	US-09-193-853-1	Sequence 1, Appli
	41	72.2	39.7	146	2	US-08-902-623-44	Sequence 44, Appli
	42	71	39.0	4411	2	US-08-929-967-5	Sequence 5, Appli
	43	71	39.0	5443	2	US-08-929-967-1	Sequence 1, Appli
	44	71	39.0	5616	2	US-08-929-967-3	Sequence 3, Appli
	45	70.8	38.9	369	4	US-09-265-919-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-217-360-16
; Sequence 16, Application US/08217360
; Patent No. 5530191
; GENERAL INFORMATION:
; APPLICANT: MALIGA, Pal
; TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC
; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESSEE: P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,360
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers University
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215)563-4100
; TELEFAX: (215)563-4044
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-217-360-16

Query Match 49.2%; Score 89.6; DB 1; Length 171;
Best Local Similarity 78.3%; Pred. No. 1.3e-21;
Matches 130; Conservative 0; Mismatches 14; Indels 22; Gaps 1;
OY 7 GCTCCCCCGCTCGTTCATGAGGCTCGTGGGATTCACGTGAGGGG 66


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RESULT 4
US-08-189-256A-19
; Sequence 19, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,256A
; FILING DATE: 31-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/111,398
; FILING DATE: 25-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-189-256A-19

Query Match 47.3%; Score 86; DB 2; Length 140;
Best Local Similarity 90.2%; Pred. NO. 2.1e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 7 GCTCCCCCGCGTCGTTCAATGAGATGGATAAGAGGCTCGTGGGATTACGCTGAGGGG 66
Db 17 GCTCCCCCGCGTCGTTCAATGAGATGGATAAGAGGCTCGTGGGATTACGCTGAGGGG 76

Qy 67 CAGGATGGCTATATTTCTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGATGGCTATATTTCTGGGAGGAACTCCGGGCGGAATTC 118

RESULT 5
US-09-193-853-19
; Sequence 19, Application US/09193853
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; Patent No. 6388168
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
; APPLICANT: Zoubenko, Oleg V.
; APPLICANT: Allison, Lori A.
; APPLICANT: Carrer, Helaine
; APPLICANT: Kanevski, Ivan
; TITLE OF INVENTION: DNA Constructs and Methods for Stably
; TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,256
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/518,763
; FILING DATE: 01-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-193-853-19

Query Match 47.3%; Score 86; DB 4; Length 140;
Best Local Similarity 90.2%; Pred. NO. 2.1e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 7 GCTCCCCCGCGTCGTTCAATGAGATGGATAAGAGGCTCGTGGGATTACGCTGAGGGG 66
Db 17 GCTCCCCCGCGTCGTTCAATGAGATGGATAAGAGGCTCGTGGGATTACGCTGAGGGG 76

Qy 67 CAGGATGGCTATATTTCTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGATGGCTATATTTCTGGGAGGAACTCCGGGCGGAATTC 118

RESULT 6
US-08-189-256A-26
; Sequence 26, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Svab, Zora
; APPLICANT: Staub, Jeffrey
```

us-09-762-105-14.rni

Mon Dec 16 13:20:23 2002

APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably
 Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS: Dan, Dorfman, Herrell and Skillman

ADDRESS: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,256A

FILING DATE: 31-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/111,398

FILING DATE: 25-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4044

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-189-256A-26

Query Match 47.3%; Score 86; DB 2; Length 164;

Best Local Similarity 90.2%; Pred. No. 2.2e-20;

Mismatches 10; Indels 0; Gaps 0;

Matches 92; Conservative

OY 7 GCTCCCCCGCGTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 66

DB 6 GCTCCCCCGCGTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 65

OY 67 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 108

DB 66 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 107

APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably
 Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS: Dan, Dorfman, Herrell and Skillman

ADDRESS: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-193-853-26

Query Match 47.3%; Score 86; DB 4; Length 164;

Best Local Similarity 90.2%; Pred. No. 2.2e-20;

Mismatches 10; Indels 0; Gaps 0;

Matches 92; Conservative

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DB 6 GCTCCCCCGCGTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 65

OY 67 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 108

DB 66 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 107

APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably
 Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS: Dan, Dorfman, Herrell and Skillman

ADDRESS: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-193-853-26

Query Match 47.3%; Score 86; DB 4; Length 164;

Best Local Similarity 90.2%; Pred. No. 2.2e-20;

Mismatches 10; Indels 0; Gaps 0;

Matches 92; Conservative

OY 7 GCTCCCCCGCGTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 66

DB 6 GCTCCCCCGCGTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 65

OY 67 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 108

DB 66 CAGGGATGGCTATATTTCTGGGAGGAGACCAACGGTTTC 107

STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/189,256A
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

Query Match 46.9%; Score 85.4; DB 2; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTCCCGCGCGTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 66
|||||
Db 23 GCTCCCGCGCGTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 82

Qy 67 CAGGATGGCTATATTTCTGGGAGGA 93
|||||
Db 83 CAGGATGGCTATATTTCTGGGAGGA 109

RESULT 9
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carter, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/193,853
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-18

Query Match 46.9%; Score 85.4; DB 4; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTCCCGCGCGTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 66
|||||
Db 23 GCTCCCGCGCGTCTCAATGAGATGAGGCTCGTGGGATTGACGTGAGGGG 82

Qy 67 CAGGATGGCTATATTTCTGGGAGGA 93
|||||
Db 83 CAGGATGGCTATATTTCTGGGAGGA 109

RESULT 10
US-08-189-256A-4
Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carter, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

us-09-762-105-14.rni

Mon Dec 16 13:20:23 2002

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA: US 07/518,763
APPLICATION NUMBER: 36,252
REGISTRATION INFORMATION:
TELEPHONE: (215) 563-4044
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-4

Query Match 46.9%; Score 85.4; DB 2; Length 165;
Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTGTTCAATGAGTGAAGAGGCTCTGGGATTCAGCTGAGGGG 66
Db 1 GCTCCCGCCGCTGTTCAATGAGTGAAGAGGCTCTGGGATTCAGCTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
Db 61 CAGGGATGGCTATATTTCTGGGAGGGA 87

RESULT 11
US-08-189-256A-4
Sequence 4, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4044
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-4

Query Match 46.9%; Score 85.4; DB 4; Length 165;
Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCCGCTGTTCAATGAGTGAAGAGGCTCTGGGATTCAGCTGAGGGG 66
Db 1 GCTCCCGCCGCTGTTCAATGAGTGAAGAGGCTCTGGGATTCAGCTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
Db 61 CAGGGATGGCTATATTTCTGGGAGGGA 87

RESULT 12
US-08-189-256A-2
Sequence 2, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrier, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-2

Query Match 46.9%; Score 85.4; DB 2; Length 168;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66
|||||
Db 1 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
|||||
Db 61 CAGGGATGGCTATATTTCTGGGAGGGA 87

RESULT 13

US-09-193-853-2

Sequence 2, Application US/09193853

Patent No. 6386168

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrier, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably

TRANSFORMING PLASTIDS OF MULTICELLULAR PLANTS AND

EXPRESSING RECOMBINANT PROTEINS THEREIN

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-2

Query Match 46.9%; Score 85.4; DB 4; Length 168;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66
|||||
Db 1 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
|||||
Db 61 CAGGGATGGCTATATTTCTGGGAGGGA 87

RESULT 14

US-09-283-419-3

Sequence 3, Application US/09283419A

Patent No. 6218145

GENERAL INFORMATION:

APPLICANT: Bogosian, Gregg

APPLICANT: O'Neil, Julia P.

APPLICANT: Staub, Jeffrey M.

TITLE OF INVENTION: Bacterial Expression Systems Based on Plastid or

MITOCHONDRIAL PROMOTER COMBINATIONS

FILE REFERENCE: MOPV040---

CURRENT APPLICATION NUMBER: US/09/283,419A

CURRENT FILING DATE: 1999-04-01

EARLIER APPLICATION NUMBER: 60/080,432

EARLIER FILING DATE: 1998-04-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 184

TYPE: DNA

ORGANISM: Nicotiana tabacum

US-09-283-419-3

Query Match 46.9%; Score 85.4; DB 4; Length 184;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 66
|||||
Db 2 GCTCCCGCGCGTTCATGAGATGAGAGGCTCGTGGGATTGACGTGAGGGG 61

QY 67 CAGGGATGGCTATATTTCTGGGAGGGA 93
|||||
Db 62 CAGGGATGGCTATATTTCTGGGAGGGA 88

RESULT 15

US-08-189-256A-24

Sequence 24, Application US/08189256A

Patent No. 5877402

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrier, Helaine

APPLICANT: Kanevski, Ivan

us-09-762-105-14.rni

Mon Dec 16 13:20:23 2002

TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-24

Query Match 46.9%; Score 85.4; DB 2; Length 258;
Best Local Similarity 98.9%; Pred. NO. 4.3e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7 GCTCCCGCGCTTCATGAGTGAATGAGAGGCTCGTGGGATTCACCTGAGGGG 66
Db 17 GCTCCCGCGCTTCATGAGTGAATGAGAGGCTCGTGGGATTCACCTGAGGGG 76
Oy 67 CAGGATGCTATATTTCTGGGAGGA 93
Db 77 CAGGATGCTATATTTCTGGGAGGA 103

Search completed: December 15, 2002, 02:07:54
Job time : 68 secs

Mon Dec 16 13:20:24 2002

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; APPLICANT: Staub, Jeffrey
; APPLICANT: Ye, Guangning
; TITLE OF INVENTION: Method for the transformation of plant cell plastids
; FILE REFERENCE: 15869WO
; CURRENT APPLICATION NUMBER: US/09/843.324A
; PRIOR FILING DATE: 2001-04-25
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-843-324A-2

Query Match      42.7%; Score 77.8; DB 10; Length 244;
Best Local Similarity 97.5%; Pred. No. 3.4e-16;
Matches 79; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCGCGTGTTCATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGGCGACAGGA 72
Db 11 CCCCCTGCTTCAATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGGCGACAGGA 70
QY 73 TGGCTATATTTCTGGGAGGGA 93
Db 71 TGGCTATATTTCTGGGAGGGA 91

RESULT 3
US-10-085-476-12
; Sequence 12, Application US/10085476
; Patent No. US20020164722A1
; GENERAL INFORMATION:
; APPLICANT: De Francesco, Raffaele
; APPLICANT: Bomei, Lucia
; APPLICANT: Behrens, Sven-Erik
; TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
; TITLE OF INVENTION: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL
; TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
; FILE REFERENCE: IT0002PCA
; CURRENT APPLICATION NUMBER: US/10/085,476
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 1998-03-23
; PRIOR FILING DATE: 1996-05-24
; PRIOR FILING DATE: 1995-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 399
; TYPE: RNA
; ORGANISM: Rattus norvegicus
US-10-085-476-12

Query Match      38.0%; Score 69.2; DB 9; Length 399;
Best Local Similarity 68.9%; Pred. No. 2.6e-13;
Matches 51; Conservative 20; Mismatches 3; Indels 0; Gaps 0;

QY 90 GGGAGACCACACGGTTCCCACTAGAAATAATTTGTTTAACTTTAAGAAGGAGATATA 149
Db 1 GGGAGACCACACGGUUUCCCUAGAAAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 60

QY 150 CATATGCCAAGCAT 163
Db 61 CAUAGGCUAGAAU 74
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RESULT 4
US-09-813-718-9
; Sequence 9, Application US/09813718
; Publication NO. US20020182866A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5018
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3428)..(4879)
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: full-length TrpRS in pET20B
US-09-813-718-9

Query Match      37.1%; Score 67.6; DB 9; Length 5018;
Best Local Similarity 94.6%; Pred. No. 2.6e-12;
Matches 70; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCACTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
Db 3364 AGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 3423
QY 149 ACATATGCCAAGCA 162
Db 3424 ACATATGCCAACA 3437

RESULT 5
US-09-987-107-51
; Sequence 51, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6 Fx Cys-Apo A1 plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(882)
; OTHER INFORMATION:
US-09-987-107-51

Query Match      36.7%; Score 66.8; DB 9; Length 1057;
Best Local Similarity 97.1%; Pred. No. 2.4e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCACTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
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Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95
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Qy 149 ACATATGGCA 158
      |||
Db 96 ACATATGGGA 105
      |||

RESULT 6
US-09-987-107-49
; Sequence 49, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Apo A-1-del 43 - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(918)
; OTHER INFORMATION:
US-09-987-107-49

Query Match 36.7%; Score 66.8; DB 9; Length 1088;
Best Local Similarity 97.1%; Pred. No. 2.5e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
      |||
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95
      |||
Qy 149 ACATATGGCA 158
      |||
Db 96 ACATATGGGA 105
      |||

RESULT 7
US-09-987-107-47
; Sequence 47, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
US-09-987-107-53

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
      |||
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95
      |||
Qy 149 ACATATGGCA 158
      |||
Db 96 ACATATGGGA 105
      |||

RESULT 9
US-09-987-107-55
; Sequence 55, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6 Trip-A-Apo A-1 - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
US-09-987-107-47

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
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Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95
      |||
Qy 149 ACATATGGCA 158
      |||
Db 96 ACATATGGGA 105
      |||

RESULT 8
US-09-987-107-53
; Sequence 53, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
US-09-987-107-53

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 148
      |||
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTTAACTTTAAGAAGGAGATAT 95
      |||
Qy 149 ACATATGGCA 158
      |||
Db 96 ACATATGGGA 105
      |||

RESULT 9
US-09-987-107-55
; Sequence 55, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
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; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26 PA2001 00057
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1068)
; OTHER INFORMATION:
US-09-987-107-55

Query Match          36.7%; Score 66.8; DB 9; Length 1238;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 10
US-09-987-107-57
; Sequence 57, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1068)
; OTHER INFORMATION:
US-09-987-107-57

Query Match          36.7%; Score 66.8; DB 9; Length 1238;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

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||||||| |
Db 96 ACATATGGGA 105

RESULT 11
US-09-987-107-59
; Sequence 59, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 final K9AK15A - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1068)
; OTHER INFORMATION:
US-09-987-107-59

Query Match          36.7%; Score 66.8; DB 9; Length 1238;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGGGAGACCACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 12
US-09-987-107-61
; Sequence 61, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 (GS)3 Trip-A-Fn-Apo A1 AmpR plasmid
; NAME/KEY: CDS

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; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-61

Query Match          36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 148
Db 36 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 13
US-09-987-107-63
; Sequence 63, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7H6 Trip-A-Tn-Apo A1-final - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-63

Query Match          36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 148
Db 36 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 14
US-09-987-107-65
; Sequence 65, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26

; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-61

Query Match          36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 148
Db 36 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 15
US-09-987-107-43
; Sequence 43, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6ubiF Apo A-1 plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1107)
; OTHER INFORMATION:
US-09-987-107-43

Query Match          36.7%; Score 66.8; DB 9; Length 1282;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 148
Db 36 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105

RESULT 16
US-09-987-107-43
; Sequence 43, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pT7 H6ubiF Apo A-1 plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1107)
; OTHER INFORMATION:
US-09-987-107-43

Query Match          36.7%; Score 66.8; DB 9; Length 1282;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 148
Db 36 AGGAGACCACACGGTTCCCTAGAAATAATTTGTTTAACCTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
Db 96 ACATATGGGA 105
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us-09-762-105-14.rnpb

Mon Dec 16 13:20:24 2002

Search completed: December 15, 2002, 03:13:31
Job time : 92 secs

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/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHLZ72"
/clone_lib="BOHL"
/notes="Vector: pHOS1; site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      215 a 139 c 184 g 249 t
ORIGIN
Query Match      39.9%; Score 72.6; DB 17; Length 787;
Best Local Similarity 85.3%; Pred. No. 2.1e-12;
Matches 81; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTGCGTCCCGCGCTGCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 63
DB 664 CTGCTCCCTCGCTGTGATGATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 723
QY 64 GGGCAGGATGGCTATATTTCTGGGAGGACCA 98
DB 724 GGGTAGGGTAGCTATATTTCTGGGAGGACTCCA 758

RESULT 2
BH424823
LOCUS      BohnJ79TR BOHN Brassica oleracea genomic clone BOHNJ79, DNA
DEFINITION
ACCESSION  BH424823
VERSION    BH424823.1 GI:17610551
KEYWORDS   GSS.
SOURCE     Brassica oleracea.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 775)
            Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
            Whole genome shotgun sequencing of Brassica oleracea
            unpublished (2001)
            Other_GSSs: BOHNJ79TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
            Location/Qualifiers
            1..775
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
            /clone="BOHLZ72"
            /clone_lib="BOHL"
            /note="Vector: pHOS1; site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      203 a 161 c 247 g 164 t
ORIGIN
Query Match      39.8%; Score 72.4; DB 17; Length 775;
Best Local Similarity 87.8%; Pred. No. 2.5e-12;
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 CTGCGTCCCGCGCTGCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 63
DB 8 CTGCTCCCTCGCTGTGATGATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 67
QY 64 GGGCAGGATGGCTATATTTCTGGGAGGGA 93
DB 68 GGGTAGGGTAGCTATATTTCTGGGAGCGA 97
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RESULT 3
BH509684
LOCUS      BOHSH07TF BOHS Brassica oleracea genomic clone BOHSH07, DNA
DEFINITION
ACCESSION  BH509684
VERSION    BH509684.1 GI:17717774
KEYWORDS   GSS.
SOURCE     Brassica oleracea.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 735)
            Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
            Whole genome shotgun sequencing of Brassica oleracea
            unpublished (2001)
            Other_GSSs: BOHSH07TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: IF
            Class: sheared ends.
            Location/Qualifiers
            1..735
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
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            /clone="BOHSH07"
            /note="Vector: pHOS1; site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      205 a 133 c 172 g 225 t
ORIGIN
Query Match      39.7%; Score 72.2; DB 17; Length 735;
Best Local Similarity 86.0%; Pred. No. 2.8e-12;
Matches 80; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 4 CTGCGTCCCGCGCTGCTCAATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 63
DB 521 CTGCTCCCTCGCTGTGATGATGAGATGAGAGGCTCGTGGGATTGACGTGAGG 580
QY 64 GGGCAGGATGGCTATATTTCTGGGAGGAGAC 96
DB 581 GGGTAGGGTAGCTATATTTCTGGGAGCGAAC 613

RESULT 4
BH472349
LOCUS      BOGIY45TF BOGI Brassica oleracea genomic clone BOGIY45, DNA
DEFINITION
ACCESSION  BH472349
VERSION    BH472349.1 GI:17680460
KEYWORDS   GSS.
SOURCE     Brassica oleracea.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 838)
            Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
            Whole genome shotgun sequencing of Brassica oleracea
            unpublished (2001)
            Other_GSSs: BOGIY45TR
            Contact: Chris Town
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DATE 2002 JAN 11 15 00:09, FROM: NO: 3105 12,

Db	697	CTTGTCCCTCCGCTGTCATGCAATAGATGATAGAGGCTCGTGGGATTGACGTGAGG	756
QY	64	GGCAGGAGTGGCTATATTTCTGGGAGGAGACCA	98
Db	757	GGTAGGGGTAGCTATATTTCTGGGAGCGAAGTCA	791
RESULT 10			
LOCUS	BH721450		
DEFINITION	BOMFRL1TR BO_2_3_KB Brassica oleracea genomic clone BOMFRL11, DNA		
ACCESSION	BH721450		
VERSION	BH721450.1	GI:18823465	
KEYWORDS	GSS.		
SOURCE	Brassica oleracea.		
ORGANISM	Brassica oleracea.		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	1 (bases 1 to 847)		
TITLE	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.		
JOURNAL	Whole genome shotgun sequencing of Brassica oleracea		
COMMENT	Unpublished (2001)		
Other_GSSs:	BOMFRL1TF		
Contact:	Chris Town		
TIGR			
9712 Medical Center Drive, Rockville, MD 20850, USA.			
Tel:	301-838-3523		
Fax:	301-838-0208		
Email:	cdtown@tigr.org		
DNA is from a doubled haploid provided by Tom Osborn.			
Seq primer:	TR		
Class:	sheared ends.		
FEATURES			
source	1..847		
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/strain="TO1000DH3"			
/db_xref="taxon:3712"			
/clone="BOMFRL1"			
/clone_lib="BO_2_3_KB"			
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"			
BASE COUNT	239 a 145 c 200 g 263 t		
ORIGIN			
Query Match	39.0%;	Score 71;	DB 17; Length 847;
Best Local Similarity	84.2%;	Pred. No. 7.1e-12;	
Matches	80; Conservative	0; Mismatches	15; Indels 0; Gaps 0;
QY	4	CTCGCTCCCGCGCTGTTCAATGGAATGGAATGGAAGGCTCGTGGGATTGACGTGAGG	63
Db	641	CTTGCTCCCTCGTGCATGATAGATGATAGATGATAGAGGCTCGTGGGATTGACGTGAGG	700
QY	64	GGCAGGAGTGGCTATATTTCTGGGAGGAGACCA	98
Db	701	GGGTAGGGGTAGCTATATTTCTGGGAGCGAAGTCA	735
RESULT 11			
LOCUS	AQ962940/c		
DEFINITION	LERGI42TR LERG Arabidopsis thaliana genomic clone LERGI42, DNA		
ACCESSION	AQ962940		
VERSION	AQ962940.1	GI:6790641	
KEYWORDS	GSS.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
1 (bases 1 to 169)			

Mon Dec 16 13:20:27 2002

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LOCUS          BH474703
DEFINITION     BOGQI49TF BOGQ Brassica oleracea genomic clone BOGQI49, DNA
ACCESSION      BH474703
VERSION        BH474703.1 GI:17682814
KEYWORDS       GSS.
SOURCE         Brassica oleracea.
ORGANISM       Brassica oleracea.
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE          Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL        1 (bases 1 to 292)
COMMENT        Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                Whole genome shotgun sequencing of Brassica oleracea
                Unpublished (2001)
                Other_GSSs: BOGQI49TR
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208
                Email: cdtown@tigr.org
                DNA is from a doubled haploid provided by Tom Osborn.
                Seq primer: TF
                Class: Sheared ends.
                Location/Qualifiers
                1..292
                /organism="Brassica oleracea"
                /strain="TO1000DH3"
                /db_xref="taxon:3712"
                /clone_lib="BOGQI49"
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                /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
                genomic DNA inserted into PHOS1 using BstXI linkers"
                83 a 50 c 79 g 80 t

BASE COUNT     83 a 50 c 79 g 80 t
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Best Local Similarity 86.7%; Pred. No. 5.3e-12;
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QY 4 CTCGCTCCCCCGCTCGTCAATGAGATGATGAAGAGCTCTGGGATTGACGTGAGG 63
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Db 58 CTGTCTCCCTCGCTGATCGAATGAAGATGATGAAGAGCTCTGGGATTGACGTGAGG 117
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QY 64 GGGCAGGAGTGCTATATTTCTGGGAGGGA 93
|| ||||| ||| || | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 118 GGGTAGGGGTAGCTATATTTCTGGGAGGGA 147
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RESULT 13
BH677595
LOCUS          BH677595
DEFINITION     BOMCM49TR BO_2_3_KB Brassica oleracea genomic clone BOMCM49, DNA
ACCESSION      BH677595
VERSION        BH677595.1 GI:18748038
KEYWORDS       GSS.
SOURCE         Brassica oleracea.
ORGANISM       Brassica oleracea.
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE          Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL        1 (bases 1 to 238)
COMMENT        Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                Whole genome shotgun sequencing of Brassica oleracea
                Unpublished (2001)
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208
                Email: cdtown@tigr.org
                DNA is from a doubled haploid provided by Tom Osborn.
                Seq primer: TR
                Class: Sheared ends.
                Location/Qualifiers
                1..238
                /organism="Brassica oleracea"
                /strain="TO1000DH3"
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                /clone="BOMCM49"
                /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
                genomic DNA inserted into PHOS1 using BstXI linkers"
                63 a 41 c 67 g 67 t

BASE COUNT     63 a 41 c 67 g 67 t
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Best Local Similarity 86.7%; Pred. No. 5.6e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4 CTCGCTCCCCCGCTCGTCAATGAGATGATGAAGAGCTCTGGGATTGACGTGAGG 63
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Db 99 CTGTCTCCCTCGCTGATCGAATGAAGATGATGAAGAGCTCTGGGATTGACGTGAGG 158
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QY 64 GGGCAGGAGTGCTATATTTCTGGGAGGGA 93
|| ||||| ||| || | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 159 GGGTAGGGGTAGCTATATTTCTGGGAGGGA 188
|| ||||| ||| || | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
BH474703
LOCUS          BH474703
DEFINITION     BOGQI49TF BOGQ Brassica oleracea genomic clone BOGQI49, DNA
ACCESSION      BH474703
VERSION        BH474703.1 GI:17682814
KEYWORDS       GSS.
SOURCE         Brassica oleracea.
ORGANISM       Brassica oleracea.
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE          Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL        1 (bases 1 to 305)
COMMENT        Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                Whole genome shotgun sequencing of Brassica oleracea
                Unpublished (2001)
                Other_GSSs: BOGWR48TF BOGWR48TR.1 BOGWR48TR
                Contact: Chris Town
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA.
                Tel: 301-838-3523
                Fax: 301-838-0208

```

Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES

source
 Location/Qualifiers
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 /organism="Brassica oleracea"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOGR48"
 /clone_lib="BO_2_3_KB"
 /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 88 a 85 c 57 g 75 t
 ORIGIN

Query Match 38.9%; Score 70.8; DB 17; Length 305;
 Best Local Similarity 86.7%; Pred. No. 6e-12;
 Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 4 CTCGCTCCCGCCGCTCGTTCATGAGATGATAGAGGCTCGTGGGATTGACGTGAGG 63
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 Db 102 CTTGCTCCCTCGCTGTGATCGATAGATGATAGAGGCTCGTGGGATTGACGTGAGG 43
 QY 64 GGGCAGGGATGGCTATATTTCTGGGAGGA 93
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 Db 42 GGGTAGGGTAGCTATATTTCTGGGAGGCA 13

Search completed: December 15, 2002, 02:06:36
 Job time : 2432 secs

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